IN THE CLAIMS:

Claim 1 (currently amended) An isolated polypeptide comprising ~~the~~ amino acid sequences selected from the group consisting of SEQ ID NOS: 2 and 4, and fragments thereof.

Claim 2 (original) The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 79 to 88 of SEQ ID NO: 2.

Claim 3 (original) The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 236 to 245 of SEQ ID NO: 4.

Claim 4 (currently amended) An isolated nucleic acid comprising ~~the~~ a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1 and 3, and fragments thereof.

Claim 5 (original) The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 314 to 319 of SEQ ID NO: 1.

Claim 6 (original) The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 304 to 333 of SEQ ID NO: 1.

Claim 7 (original) The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 790 to 795 of SEQ ID NO: 3.

Claim 8 (original) The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 775 to 804 of SEQ ID NO: 3.

Claim 9 (original) An expression vector comprising the nucleic acid of Claim 4.

Claim 10 (original) A host cell transformed with the expression vector of Claim 9.

Claim 11 (currently amended) A method for producing ~~the~~ a polypeptide ~~of Claim 1~~, which comprises the steps of:

(1) culturing the host cell of Claim 10 under a condition suitable for the expression of the polypeptide; and

(2) recovering the polypeptide from the host cell culture.

Claim 12 (original) An antibody specifically binding to the polypeptide of Claim 1.

Claim 13 (currently amended) A method for diagnosing ~~the diseases~~ a disease associated with ~~the~~ a deficiency of ~~the~~ an ARL gene in a mammal, ~~in particular cancers,~~ which comprises detecting the nucleic acid of Claim 4 or ~~the~~ a polypeptide encoded thereby ~~of Claim 1~~.

Claim 14 (currently amended) The method of Claim 13, wherein the detection ~~of the nucleic acid of Claim 4~~ comprises the steps of:

(1) extracting total RNA from a sample obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) to obtain a cDNA sample;

(3) bringing the cDNA sample into contact with the nucleic acid ~~of Claim 4~~; and

(4) detecting whether the cDNA hybridizes with the nucleic acid ~~of Claim 4~~.

Claim 15 (original) The method of Claim 14 further comprising the step of determining the amount of hybridized sample.

Claim 16 (currently amended) The method of Claim 13, wherein the detection of the nucleic acid ~~of Claim 4~~ comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotide 314 to 319 of SEQ ID NO: 1 or nucleotide 790 to 795 of SEQ ID NO: 3; and

(3) detecting whether the cDNA is obtained.

Claim 17 (currently amended) The method of Claim 13, wherein the detection of the nucleic acid ~~of Claim 4~~ comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain

reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotide 304 to 333 of SEQ ID NO: 1 or nucleotide 775 to 804 of SEQ ID NO: 3; and

(3) detecting whether the cDNA is obtained.

Claim 18 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 314 to 319 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 319, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 314 to 319 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 314.

Claim 19 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 304 to 333 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 333, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 304 to 333 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 304.

Claim 20 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 790 to 795 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the

nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 795, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 790 to 795 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 790.

Claim 21 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 775 to 804 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 804, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 775 to 804 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 775.

Claim 22 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 314 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 319.

Claim 23 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations

upstream of nucleotide 790 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 795.

Claim 24 (original) The method of Claim 22, the cDNA sample amplified from SEQ ID NO: 1 is 247bp shorter than that from ARL.

Claim 25 (original)The method of Claim 23, the cDNA sample amplified from SEQ ID NO: 3 is 58bp shorter than that from ARL.

Claim 26 (original) The method of Claim 16 further comprising the step of detecting the amount of the amplified cDNA sample.

Claim 27 (currently amended) The method of Claim 13, wherein the detection of the polypeptide ~~of Claim 1~~ comprises the steps of contacting ~~the~~ an antibody that specifically binds to the polypeptide ~~of Claim 12~~ with protein samples extracted from the mammal, and detecting whether an antibody-polypeptide complex is formed.

Claim 28 (original) The method of Claim 27 further comprising the step of determining the amount of the antibody-polypeptide complex.